



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Sequence-Directed DNA Binding
Molecules, Compositions and Methods

(iii) NUMBER OF SEQUENCES: 664

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(B) FILING DATE: 20-DEC-1993

(viii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 17-SEP-1993

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(B) FILING DATE: 27-JUN-1991

(viii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 22-JUN-1993

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(C) REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ferredoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTGCTTG CCAATGTCTT TATAGGTCAC CCGGAAGGCA CG

42

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human macrophage alphas-antitrypsin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTACTGCCT CCACCCGAAG TCTACTTCCT GGGTGGGCAG GAAC

44

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene B for alpha 1-acid
glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGTGACCGCC CATAGTTTAT TATAAAGGTG ACTGCACCCT GCAGCC

46

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha 1
microtubulin-bikunin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATTGGAGCTG TCCTTGGGGC TGTAATTGGC CCCAGCTGAG CAGGGCA

47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha-2 macroglobulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTGCAC ACAGAGCAGC ATAAAGCCCA GTTGCTTTGG GAAGT

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTCGGGTTTG GCTACAAAAG GTGGAAAGAC TTCCGGTCTG CATTCTTG

48

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGGTAGGC GGGGCATTGA GTGGAAAGCT CGGCTGGGCG GTGCCTGT

48

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAATTGTGA CCCACAGCCT AATAATAACA GTCTTTGCCC TCTTGGCC

48

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human angiotensin I-converting enzyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGGGGGTG TGTCGGGTTT TATAACCCGC AGGGCGGCCG CGGCG

45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene fragment for the acetylcholine receptor gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGTGGGAG TGTAGGCTGT TATATGACAC CCAGAGCCCA TCTCT

45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human cytokine (Act-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCCTAGGCC TCAGAGTCCC TATAAAGAGA GATTCCCAAC TCAGTA

46

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGAGTGAG CGGCGCGGGG CCAATCGCGT GCGCCGTTCC GAAAG

45

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGGCCGC GGCGGCGCCC TATAAAACCC AGCGGCGCGA CGCGCCA

47

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cardiac actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCCAACT GACCCTGTCC ATCAGCGTTC TATAAAGCGG CCCTCCTGGA

50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for vascular smooth muscle alpha-actin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGAGAGCA GGCCAAGGGC TATATAACCC TTCAGCTTTC AGCTTCC

47

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human enteric smooth muscle gamma-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGATCCGCC TCTGGGGTTT TATATTGCTC TGGTATTCAT GCCA

44

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human arachidonate 12-lipoxygenase gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGGGCCGC AGACCGGTCC TTAAAGGTT GGAAGTGGCC CCGAGG

46

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alcohol dehydrogenase alpha subunit (ADH1) gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTGTATTC AAGCAAAAAA AATAAATAAA TACCTATGCA ATACACCT

48

- (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta subunit gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGTTACAC AAGCAAACAA AATAAATATC TGTGCAATAT ATCTGCTT

48

- (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTCAGC ATGATTTTCC

50

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human cytosolic adenylate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGCCGCGCG CTGACAGCCT TATAAATAGT CGCCTTTGCC GGCCGCC

47

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-N-acetylgalactosaminidase (AK1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGACTTATC AGGTTACCGG ATTCGAGTCA GAAGCGGCGG CAGGTCTGAA

50

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ALAD gene for porphobilinogen synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATAAAGACCT TTGATCGGAT CTATCATTGT ACCTATCATA GGTCTG

46

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ALAD gene for porphobilinogen synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCCTACCAAG GAGGAAGACT GGATAAAATG GCCTGAGATG GCTGAA

46

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGTGACA AAGGCCTGAA TTTGTCAATT AGTAACAATT GTATTCAACA GTAAGGAT

58

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTGCTCACCA CACACAAGTG TTATAGGAGG AGTCTGGCCC TTGAG

45

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase C gene for fructose 1,6-bisphosphate aldolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACCTGCAATA CCCCCTTACC CCAATACCAA GACCAACTGG CATAG

45

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCATAGAGC CAACTGAGAT AAATGCTATT TAAATAAAGT GTATTTAATG AATTTCTCCA 60

AGCTTACGGA 70

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCCACACG TCAACGATTC TATTTGAAGT TGGGCAGGGG GTGGC 45

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTAGAGAAG ATCGGGGACA CATGTGGGGC TGGGCAGGAG CTG 43

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGGCTGGGCA GGAGCTGCCT TATAACCACC CGGGAACCCC TAGCT

45

- (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCGGAGGGCG GAGTGGTGCC TTAAAGGC CGGCGCCGCC TTCCGC

46

- (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGCGCCGCCC CTTCCGAGGC TAAATCGCTT CCTCTCGGAA CGCGC

45

- (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAAAAACATG ATGAGAAGTC TATAAAAATT GTGTGCTACC AAAGA

45

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukemia inhibitory factor
(LIF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTTACAACAC AGGCTCCAGT ATATAAATCA GGCAAATTCC CCATTTGAGC

50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aminopeptidase N gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGCTCCTC CCCTTTGGGG ATATAAGCCC GGCCTGGGGC TGCTCC

46

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAATGTGCTT CTTACAGGAA TATAAATAGT TTCTGGAAAG GACACTG

47

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG

47

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT

54

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human amyloid-beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCGGGGTGGG CCGGATCAGC TGACTCGCCT GGCTCTGAGC CCCGCCG

47

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human amyloid-beta protein (APP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCAGCTGACT CGCCTGGCTC TGAGCCCCGC CGCCGCGCTC GGGCTCCGTC

50

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pronatriodilatin precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGCTTGGAGA GCTGGGGGGC TATAAAAAGA GGCGGCACTG GGCAGC

46

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTGAAGTGGG AGCCTCTTGA GTCAAATCAG TAAGAATGCG GCTCTTGCA

49

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGCGGATGA TAACTTTAAA AGGGCATCTC CTGCTGGCTT CTCACTTGG

49

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGCTTGGAGA GCTGGGGGGC TATAAAAAGA GGCGGCACTG GGCAGC

46

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTTGGAGAGC TGGGGGGCTA TAAAAAGAGG CGGCACTGGG CAGCTGGGAG

50

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human angiotensinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCCATCCCC ACCCCTCAGC TATAAATAGG GCCTCGTGAC CCGGCC

46

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human heart/skeletal muscle ATP/ADP
translocator gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGCGAGAGC CCGGCGGGGA TATAAGGGGG AGCTGCGGGC CAGGC

45

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCTGGACACC CTGCCTCAGG CCCTCATCTC CACTGGTCAG CAGGTGACC

49

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC CCAGCGCCC

49

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC

48

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACACCCTGC CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC

50

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC

48

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATAATCCCTG CCCCACTGGG CCCATCCATA GTCCCTGTCA CCTGACAGG

49

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGGTGGGTA AACAGACAGG TATATAGCCC CTTCTCTCC AGCCAG

46

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fetal gene for apolipoprotein
AI precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGCAGACAT AAATAGGCCC TGCAAGAGCT GGC

33

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCCTGGGCTT CCTATAAATG GGGTGCGGGC GCCGGCCGC

39

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apoC-II gene for
preproapolipoprotein C-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGAAGTGGG TCTCAACCAC TATAAATCCT CTCTGTGCCC GTCCGGA

47

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein C-I (VLDL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGCCCCGCCC CTCCCCAGCC TGATAAAGGT CCTGCGGGCA GGACAGG

47

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein D gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCAGAGACC TGAAGAAGCT TATAAAATAG CTTGGGAGAG GCCAGTC

47

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human arginase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGTTGTTTAT TCAACCCAAG TATAAATGGA AAAAAAAGAT GCGCC

45

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human argininosuccinate synthetase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCCCCCGG GCCCTGTGCT TATAACCTGG GATGGGCACC CCTGC

45

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha 3 subunit (ATP1 A3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCCTCCCGC GGACGCGGGC ATATGAGGAG GCGGAGGCGG CGGC

44

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human (BSF-2/IL6) gene for B cell stimulatory factor-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTAGAGTCT CAACCCCCAA TAAATATAGG ACTGGAGATG TCTGAGGC

48

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human C5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTGAATTCT TCAAGTTCAG TTTATTTAAA AGGAGACTAT CCTCAAAAGT G

51

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CCTCCCCCTTG TCGCCTAGGT CCACCCGAGC CCCCTCCCCC GGGCC

45

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACGAAGTT GGCGGGAGCC TATAAAAGCG GGCCGGCGCG ACCCGC

46

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human calcitonin/alpha-CGRP gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCCCGACCC ACAGCGGCGG GAATAAGAGC AGTCGCTGGC GCTGG

45

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human calretinin gene, exon 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGCGCAGG CTCCAGAGCG TATATAAGGG CAGCGTGGCG CACAACC

47

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cathepsin G gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTCCTTCCTC TCTCAGGGCC TTAAAGTCTA GGAGGAGGAA GCACA

45

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase VII (CA VII) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTCCTCCCGC CAGCCGCTGC TTTAAGAGGC TGCTCCGCGG TAGCG

45

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCTAGTGACA ACAGCCCTTT CTAAATCCGG CTAGGGACTG GGTGCC

46

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TGGGGGTGCC TGCTGCCCCA TATATACAGC CCCTGAGACC AGGTC

45

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human complement C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGGGGGAAAG CAGGAGCCAG ATAAAAAGCC AGCTCCAGCA GGCGCTG

47

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human recognition/surface antigen
(CD4) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAGTCCTCA CACAGATACG CCTGTTTGAG AAGCAGCGGG CAAGAAAGAC

50

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hyaluronate receptor gene
(CD44)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TAGGTCACTG TTTTCAACCT CGAATAAAAA CTGCAGCCAA CTTCCGAGGC

50

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane
 conductance reg. gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AATGACATCA CAGCAGGTCA GAGAAAAAGG GTTGAGCGGC AGGCACCCAG 50

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE: - - - - -
 (C) INDIVIDUAL ISOLATE: Human cholesterol
 7-alpha-hydroxylase (CYP7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGATCTGG ATACTATGTA TATAAAAAGC CTAGCTTGAG TCTCTT 46

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCAATTGTG ACCCACAGCC TAATAATAAC AGTCTTTGCC CTCTTGGCC

49

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human mast cell chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCTCTTGCC TTCTAGGAGT TATAAAACCC AAGACTGGAA AGGAAA

46

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human heart chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CCTCTCTTGC CTTCTGGGAG TTATAAAACC CAAGACTGGA AGGAAAA

47

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human creatine kinase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCCAATGGA ATGAATGGGC TATAAATAGC CGCCAATGGG CGGCCCGC

48

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human C-type natriuretic peptide gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACATCAGCGG CAGGTTGGAT TATAAAGGCG CGAGCAGAGT CACGGG

46

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTCCGCGCG GGGGTGGAGG GAGAGGAGGA GGTTCCTGCC GAGGT

45

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGGGCAAGG GCATCCTGAG GGGCGGGGCC GGGGGCGGAG CCTTGC

46

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATCCTGAGGG GCGGGGCCGG GGGCGGAGCC TTGCGGGCTG GAGCGA

46

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGAGGGGCGG GGCCGGGGGC GGAGCCTTGC GGGCTGGAGC GAAAGAATGC

50

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myeloid specific CD11b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCCCTCTTCC TTTGAATCTC TGATAGACTT CTGCCTCCTA CTTCTC

46

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cholesteryl ester transferase
protein (CETP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGGGGCTG GCGGACATA CATATACGGG CTCCAGGCTG AACGGC

46

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane
conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGGTGGGGG GAATTGGAAG CAAATGACAT CACAGCAGGT CAGAG

45

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGGGGGGAA TTGGAAGCAA ATGACATCAC AGCAGGTCAG AGAAAAA

47

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human coseg gene for vasopressin-neurophysin precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CACGGGAACA CCTGCGGACA TAAATAGGCA GCCAGCAGAG GCAGCA

46

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human creatine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TTCAGAGAAA GGCAGGTGC TATAAAGGGC CCAGCGCCAC GGCCT

46

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-B-crystallin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGAAGCTTCA CAAGACTGCA TATATAAGGG GCTGGCTGTA GCTGCAG

47

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTGGGGGAA AGCAGAGCCA GATAAAAAGC CAGCTCCAGC AGGCGCTGCT

50

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human colony stimulating factor
CSF-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCCTGGCCAG GGTGATTTC CATAAACCAC ATGCCCCCA GTCCTC

46

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytotoxic serine proteinase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTACTCAGC AGCAGGGGTG TAAATGTGAC AGTGCCATGT CAAC

44

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human CST3 gene for cystatin C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGCGGCGAAG GCCGGAAGGG ATAAAACCGC AGTCGCCGGC CTCGCG

46

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human CST4 gene for Cystatin D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTGGGGGACA CCCAAGTAGG ATAAATGCAC AGCTAGCTTC TGGCC

45

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome P-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ACTAAATTAG CAGGGAGTGT TATAAAACT TTGGAGTGCA AGCTC

45

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human cholesterol desmolase cytochrome gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCAGGAGGA AGGACGTGAA CATTTTATCA GCTTCTGGTA TGGCC

45

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cholesterol desmolase
cytochrome P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAGG

46

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human steroid 11-beta-hydroxylase
(CYP11B1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAAGGCAAGG CACCAGGCAA GATAAAAGGA TTGCAGCTGA ACAGGGT

47

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human CYPXI gene for steroid
18-hydroxylase (P-450 C18)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CAGAGCAGGT TCCTGGGTGA GATAAAAGGA TTTGGGCTGA ACAGGGT

47

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human CYPXIX aromatase P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TGGACAATAA ATGAAATCTC CATAAAAGGC CCAAAGGACA GGGTTC

46

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human decay-accelerating factor (DAF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGCCCAGACC CCGCCCAAAG CACTCATTTA ACTGGTATTG CGGAGC

46

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ACGTCCATGT GTCATTAGTG CCAATTAGAG GAGGGCAGCA GGCTG

45

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ACCCCATTC A GGACCAGGGC ATAAATGGCC AGGTGGGACC AGAGAG

46

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human desmin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGGGCTGATG TCAGGAGGGA TACAAATAGT GCCGACGGCT GGGGGC

46

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytokeratin 8 (CK8) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CCCGGGGCTG GGATCTCTTT TATAAAAGGC CATTCTGAG AGCTC

45

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human DNA polymerase alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCTCCCGAG CCGCTGATTG GCTTTCAGGC TGGCGCCTGT CTCGGCCCCC

50

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human dopamine D1A receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCTGTGCCCC GCGGGAACCC CGCCGGCCTG TGCGCTTGCT GGTGCCAGCT

50

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human eosinophil cationic protein
(ECP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGACCCACCA AGGGAAGCTT TATTTAAACA GTTCCAAGTA GGGGAGA

47

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human HER2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAGGAGGAGG GCTGCTTGAG GAAGTATAAG AATGAAGTTG TGAAGCTGAG

50

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human elastin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGTCTCGCT GTGATAGATC AATAAATATT TTATTTTTTG TCCTGG

46

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human endothelial leukocyte adhesion
molecule I (ELAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATTACACAGGA AGCAATCCCT CCTATAAAAG GGCCTCAGCC GAAGTAGTG

49

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human eosinophil major basic protein
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGAAGTTCCT CCAAGGCCTC TATATAAGAA GTCTTTGTGA GAGGAAG

47

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCTAGGAAA GTTCTCAGC TCTCAAACCT CTGTTTTCTC ATCTGCAAG

49

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTCTCATCTG CAAGATGGGG ATAATATTAA CCAACTGGCT AGGTCATGAG

50

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ENO3 gene for muscle-specific enolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGGGACCGAG TGGCTCAGGG ATAAATGCGC ACCTGAGAGG GGGTGA

46

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human eosinophil derived neurotoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CAACCCACCA AGGGATGCTT TATTTAAACA GTTCCAAGTA GGGGAGA

47

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human erythropoietin receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TACCCAGGCT GAGTGCTGGC CCCGCCCCCT CGGGGATCTG CCACTT

46

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-erb B2/neu protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AGGAGGGCTG CTTGAGGAAG TATAAGAATG AAGTTGTGAA GCTGA

45

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCGATTGGCT CTGCCCTAGC GGATTGACGG GCAGGTTAGC CAATGGTCT

49

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CAGGTTAGCC AATGGTCTCG TAATATAGGT GGAGCGAGCC CTCGAGG

47

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human erythropoietin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACCCGG CGCGCCCCAG GTCGCTGAGG GACCCCGGCC AGGCGCGGAG

50

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human oestrogen receptor

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATATGAGCTC GGGAGACCAG TACTTAAAGT TGGAGGCCCG GGAGCCCA

48

- (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human elastase I gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGCTTTGCTG CTAAGAGGAG TATAAAGAGG GCTTGGTCCA AGCAAG

46

- (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCCCCGTGA TCAGCTCCAG CCATTTCAG TCCTGGCTAT CCCA

44

- (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA

45

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TTAACATCTC TAGTTCTCAC CCAATTCTCT TACCTGAGAA ATGGA

45

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GTTATCCGGG TGGCAAGCCC ATATTTAGGT CTATGAAAAT AGAAGCT

47

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AGCCCATATT TAGGTCTATG AAAATAGAAG CTGTCAGTGG CTCTAC

46

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apoferritin H gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGCCTGACG CCGACGCGGC TATAAGAGAC CACAAGCGAC CCGCA

45

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TATTAAGTAA GGAAAGGTAA CCATTTCTGA AGTCATTCCT AGCAGA

46

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATTCCTAGCA GAGGACTCAG ATATATATAG GATTGAAGAT CTCTCAGTT

49

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CCAGAAGTAA ATACAGCTCA GCTTGTA CTT TGGTACA ACT AATCGACCTT

50

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human FK506 binding proteins 12A, 12B, and 12C (FKBP12)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAGCCGTGGA ACCGCCGCCA GGTCGCTGTT GGTCCACGCC GCCCCTCGCG

50

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human 5-lipoxygenase activating protein (FLAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TTGTGCCGGG GATCTTCAGA AATTGTAATG ATGAAAGAGT GCAAGCTCTC

50

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human fos proto-oncogene (c-fos)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATTCATAAAA CGCTTGTTAT AAAAGCAGTG GCTGCGGCGC CTCGTACTCC

50

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human GOS2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGCGTGTCTC AGAGAAAAGA TATAAGCGGC CCCCGGACGC TAAAG

45

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human granulocyte colony-stimulating factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CAGGCCTCCA TGGGGTTATG TATAAAGGGC CCCCTAGAGC TGGGCC

46

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human EGR2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CGGGTATTGA AGACCTGCCC ATAAATACTT AGAGCAACAC TTTCCGTC

48

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human growth hormone (hGH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGGGAGAGAA GGGGCCAGGG TATAAAAAGG GCCCACAAGA GACCAG

46

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gastric inhibitory polypeptide (GIP) mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TAATCAGCAG GTCTATGCCT AATATAAAGG AGCTGGGGCA TGATTTCTTC

50

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human GLA gene for alpha-D-galactosidase A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAAACAATAA CGTCATTATT TAATAAGTCA TCGGTGATTG GTCCGC

46

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTTACAGATG AGAAATTTAT ATTGTCAGCG TAATATCTGT GAGG

44

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCTAAACAG AGCTGGAGAG TATATAAAAG CAGTGCGCCT TGGTGCA

47

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human granulocyte-macrophage colony
stimulating factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CATTAATCAT TTCCTCTGTG TATTTAAGAG CTCTTTTGCC AGTGAGC

47

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucocorticoid receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TGGGCAATGG GAGACTTTCT TAAATAGGGC TCTCCCCCA CCCATG

46

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human growth hormone releasing
factor (GRF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AACGCTTAGG AAAATGAAGA GATAAATGAT GGGAACGCCA GGCGGCTGCC

50

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human GST pi gene for glutathione
S-transferase pi

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGCGGGGCG GGACCACCCT TATAAGGCTC GGAGGCCGCG AGGC

44

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: human glycophorin C (GPC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAGAAGTGGG CGGGTGTGTG TTTAAAAAAA AAAAAAGGGG TGGAAAC 47

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human histone (H10) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CGCGGTCCGC CCGCCGCCGC TAAATACCCG GATGCGCCGC CCAAGC 46

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for H1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTGGAT TTGGGAATCT TATAAGTTCT GTATGAGACC ACTC 44

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H1 histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCGGTGGAT TGGACGCTCC ACCAATCACA GGGCAGCGCC GGCTTA

46

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

- ACCAATCACA GGGCAGCGCC GGCTTATATA AGCCCGGGCC CGAGCATAGC AGCA

54

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H2B.2 and H2A.1 genes for
Histone H2A and H2B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TTTTCGCGCC CAGCAGCTGC TATAAAATGC GCGTCCCTGT AGGTTCC

47

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human H4/a gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGGGGCAGGG GTAACGTAGA TATATAAAGA TCGGTTTCCT ATTCTCTC

48

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human H4/b gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTGCAAGTAT AGTGTGTGTG TATATATATA TATATACCTA GCAGTATTTA TTAAAT

56

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human androgen receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGTGGGGGCG GGACCCGACT CGCAAACTGT TGCATTTGCT CTCCACCTCC

50

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin (hCG)
beta subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GCCCTCTCTC ATTGGGCAGA AGCTAAGTCC GAAGCCGCGC CCCTCCTGG

49

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human islet amyloid polypeptide
(hIAPP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGCAAA

50

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTCCCGCCG GCGCGCTTTC GGTITTTCAAT CTGGTCCGAT ATCTCTGTAT AT

52

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

AATCTGGTCC GATATCTCTG TATATTACGG GGAAGACGGT GACGCTC

47

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TCCTCTTTTC TTGGCGAACT CAACTGGTAT GAATTCCTCA

40

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CACAGCCTAC CTCCAGTCAG TATAAATACT TCTCTGCCTT GCGTTC

46

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TATTTGCATA AGCGATTCTA TATAAAAGCG CCTTGTCATA CCCTGCT

47

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ATTTTTGAAT TTTCTTGGGT CCAATAGTTG GTGGTCTGAC TCTAT

45

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H3 gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CAATAGTTGG TGGTCTGACT CTATAAAAGA AGAGTAGCTC TTTCCTT

47

- (2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-A1 gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AGTGTCGTCG CGGTCGCTGT TCTAAAGTCC GCACGCACCC ACCGG

45

- (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-B27 antigen gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

AGTGTCGCCG GGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCGG

46

- (2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human HLA-Bw57 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AGCGTCGCCG CGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCG

45

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human HLA-F gene for human leukocyte antigen F

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TGTCGCCGCA GTTCCCAGGT TCTAAAGTCC CACGCACCCC GCGGGA

46

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for histocompatibility antigen HLA-A3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGTGTGTCG CGGTGCTGT TCTAAAGCCC GCACGCACCC ACCGGG

46

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for class I histocompatibility antigen HLA-CW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CATTGGGTGT CGGACCTCTA GAAGGCCGGT CAGCGTCTCC GC

42

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human HMG-17 gene for non-histone chromosomal protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CGGTCCGGGG CTCCCAGCGC TATAAAACT TTATAAACCC CCCGGA

46

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human HOX3D gene for homeoprotein HOX3D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAGAAAGAGA TATCTCCACC TATAAATTGT CCACTTTGGA GAACAA

46

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human 71Kd heat shock cognate protein (hsc70)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TGGAAGGTTC TAAGATAGGG TATAAGAGGC AGGGTGGCGG GCGGA

45

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human heat shock protein (hsp 70) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AAGGCGGGTC TCCGTGACGA CTTATAAAAG CCCAGGGGCA AGCGGTCCGG

50

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CTTCGGTCTC ACGGACCGAT CCGCCCGAAC CTTCTCCCGG GGTCAG

46

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCGCCCCGGCT GACTCAGCCC GGGCGGGCGG GCGGGAGGCT CTCGAC

46

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CCGGCTGACT CAGCCCGGGC GGGCGGGCGG GAGGCTCTCG ACTGGG

46

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTGACTCAGC CCGGGCGGGC GGGCGGGAGG CTCTCGACTG GGC GGG

46

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGGCGGGCGG GAGGCTCTCG ACTGGGCGGG AAGGTGCGGG AAGGT

45

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CGGCGGGGTC GGGGAGGTGC AAAAGGATGA AAAGCCCGTG GACGGAGCTG AGC

53

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human IAPP gene for islet amyloid polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGC

47

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGGTTTCCGG GAAAGCAGCA CCGCCCCTTG GCCCCCAGGT GGCTAG

46

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GGCCCCCAGG TGGCTAGCGC TATAAAGGAT CACGCGCCCC AGTCGA

46

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interferon-inducible gene
IFI-54K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AAAGGAACCA GAGGCCACTG TATATATAGG TCTCTTCAGC ATTTATTG

48

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ATGGAAGCTA GTATGTTCTT TATTTAAGAC CTATGCACAG AGCAAGGT

48

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAAATTAGTA TGTTCACTAT TTAAGAACTA TGCACAGAGC AAAGT

45

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGAAACTC GTATGTGACC TTTTAAAGAT CTGTGCACAA AACAAGGT

48

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

ATGGAAACTA GTATGTTCCC TATTTAAGAC CTACACATAA AGCAAGGT

48

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

ATGGAAATTA GTATGTTTAC TATTTAAGAC CTATGCACAG AGCAAAGT

48

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human immune interferon (INF-gamma) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TCCTCAGGAG ACTTCAATTA GGTATAAATA CCAGCAGCCA GAGGAGGTGC

50

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha/beta-interferon (IFN)-inducible 6-16 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GGGAGGATCC ACAAGTGATG ATAAAAAGCC AGCCTTCAGC CGGAG

45

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human insulin like growth factor II

(IGF-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGGAGGAG TCGGCTCACA CATAAAAGCT GAGGCACTGA CCAGCCT

47

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human insulin-like growth factor binding protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GTGGCGCGGC CTGTGCCCTT TATAAGGTGC GCGCTGTGTC CAGCG

45

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germline leader peptide and variable region of 1154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAACCTCCTG CACTGAAGCC TTATTAATAG GCTGGCCACA CTTTCATGC

48

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human germline for leader peptide &
variable region of 2908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CAACCTCCTG CCCTGAAGAC TTATTAATAG GCTGGACACA CTTCATGC

48

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human rearranged kappa
immunoglobulin subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCACGACCAG GTGTTTGGAT TTTATAAACG GGCCGTTTGC ATTGTGAA

48

(2) INFORMATION FOR SEQ-ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human rearranged kappa
immunoglobulin gene subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CGCCCTGCAG TCCAGAGCCC ATATCAATGC CTGGGTCAGA GCTCTGGA

48

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germline fragment for immunoglobulin kappa light chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TGCCCTACCT TCCAGAGCCC ATATCAATGC CTGTGTCAGA GCCCTGGG

48

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germline immunoglobulin kappa light chain V-segment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ACTTCCCTTG TGGGTCTGAG ATAAAGCTC AGCTCTAACC CTTACC

46

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TATTTTCCA GAATTAACAG TATAAATTGC ATCTCTTGTT CAAGAG

46

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for interleukin 1 alpha (IL-1 alpha)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CCACGCCTAC TTAAGACAAT TACAAAAGGC GAAGAAGACT GACTCAG

47

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TTGATTGTGA AATCAGGTAT TCAACAGAGA AATTTCTCAG CCTCCTAC

48

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTACTTCTGC TTTTGAAAGC TATAAAAAACA GCGAGGGAGA AACTGGC

47

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AGAAAGGATT CATAAATGAA GTTCAATCCT TCTCATCACC CCAGCCCA

48

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TTTGAAAAAT TACCGCAAAC TATATTGTCA TCAAAAAAAAA AAAAAA

46

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ATCTGGTGTA ACGAAAATTT CCAATGTAAA CTCATTTTCC CTCGG

45

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GGTTTCAGCA ATTTTAAATC TATATATAGA GATATCTTTG TCAGCATT

48

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 5 (IL-5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CATTTCCTCA AAGACAGACA ATAAATTGAC TGGGGACGCA GTCTTGACT

50

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 7 (IL-7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TTGCTTTGAT TCAGGCCAGC TGGTTTTTCT GCGGTGATTC GGAAATTCGC

50

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 9 gene (IL-9)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TTCCGTGTTT GAGAGGGAGC TTAAATACC ACTCGATTG AAGGTGTC

48

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human int-1 mammary oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACTTCAGCCA GCGCCGAAC TATAAGAGGC GGTGCCGCC GCCGT

45

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human jun-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TCCGTGGCTG ACTAGCGCGG TATAAAGGCG TGTGGCTCAG GCTGAG

46

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human DNA for 65 kD keratin type II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCCCAACAAC CTCCTCAAAT GTATATAAAG GGATTTTAT TGCACA

46

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ultra high-sulphur keratin
protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGGTGTGTTC CTATGTGGGA TATAAAGAGC CGGGGCTCAG GGGGCT

46

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-lactalbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCTGAGGCTT TCTGCATGAA TATAAATAAA TGAACTGAG TGATGCT

47

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human LAG-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GTCCTAGGCC TCAGAGTCCC TATAAGAGAG ATTCCCAACT CAGTA

45

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human lecithin-cholesterol acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTGAGGCTGT GCCCCTTTCC GGCAATCTCT GGCCACAACC CCCACTGG

48

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lecthin-cholesterol
acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CCCCTCCCAC TCCACACCA GATAAGGACA GCCCAGTGCC GCTTT

45

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lymphocyte-specific protein
kinase (lck) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGGAGCAGAT CTTGGGGGAG CCCCTTCAGC CCCCTCTTCC ATTCCCTCAG

50

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukocyte fuction-associated
antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGGTATCTCA CTGTGGTTTG ATTTGCATTT CTCTAATGAC TAATAGTG

48

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human leukocyte function-associated antigen-1 (LFA-1) gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGTCTCTAA CTTGCTTACA CTTCTCCCT GAACCCTGCG GTTTCA

46

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human leukocyte function-associated antigen-1 (LFA-1) gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TCCTGCAGGC ACACCTCCCT CCCCCTGC CAGTGTACC AGCCTGTT

48

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human leukocyte function-associated antigen-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CTGTTGCCTC TGTGAGAAAG TACCACTGTA AGAGGCCAAA GGGCATGATC

50

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human lipoprotein lipase (LPL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TATTGCATA TTTCCAGTCA CATAAGCAGC CTTGGCGTGA AAACAGT

47

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukocyte adhesion molecule-1
(LAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TGGGTTAGAG AAATGAAAGA AAGCAAGGCT TTCTGTTGAC ATTCAGTGCA

50

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lysozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAAGGAAGT TAAAAGATGT TAAATACTGG GGCCAGCTCA CCCTGG

46

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mannose binding protein 1
(MBP1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

AGGGATGGGT CATCTATTTT TATATAGCCT GCACCCAGAT TG TAGG

46

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mast cell carboxypeptidase A
(MC-CPA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CATCAAGATA AGGGCTGAGG CATAAACTG CCAGAGGGTC TCAAGG

46

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human P-glycoprotein (MDR1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTTTGCCACA GGAAGCCTGA GCTCATTCGA GTAGCGGCTC TTCCA

45

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human bone marrow serine protease gene (medullasin)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

ACGGCCTCCC AGCACAGGGC TATAAGAGGA GCCGGGCGGG CACGG

45

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human microsomal epoxide hydrolase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TTGCTGTGCA GAGTCCAGGG GAGATAACCA CGCTGTGCAC ACATGAG

47

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein-Ie gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCAGCCAGTT GCAGGGCTCC ATTCTGCTTT CCAACTGCCT GACTGCTTGT TC

52

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myoglobin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TTGTCAAGCA TCCAGAAGG TATAAAAACG CCCTTGGGAC CAGGCA

46

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human melanoma growth stimulatory activity (MGSA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GCTTTCAGC CCCAACCATG CATAAAAGGG GTTCGCGGAT CTCGGAG

47

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-MHC gene for myosin heavy chain (N-terminus)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AGAGGGTGGG GGAAACGGGA TATAAAGGAA CTGGAGCTTT GAGGAG

46

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human class II invariant gamma-chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GATTCCTCTC CAGCACCGAC TTTAAGAGGC GAGCCGGGGG GTCAG

45

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human motilin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CCCAGGGTTG GGAGGTATAT AAGAACCCGT CAGATCAGCC G

41

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human myeloperoxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCACCCCCAG CTTAGAGGAC ATAAAAGCGC AGATTGAGCT AAGAGGAGCT

50

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human mitochondrial RNA-processing
endoribonuclease RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

AAACACAATT TCTTTAGGGC TATAAAATAC TACTCTGTGA AGCTGAGGA

49

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human myc-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAGGGAGGGA TCGCGCTGAG TATAAAAGCC GGTTTTTCGGG GCTTTAT

47

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Na,K-ATPase beta subunit (ATP1B) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GCACGGCCGC CGGGGCGCGG TATATAGTAA AGGTAGGGCG GGCGCA

46

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human neuromedin K receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAAGCGTGGG ACCCCATGAG TATAAAGAGA GCCTGTAGCG CAGG

44

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for heavy neurofilament subunit (NF-H) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGACCCGG CCGCGGCGGC TATAAAAGGG CCGGCGCCCT GGTCGT

46

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human nuclear factor NF-IL6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CGGTTGCTAC GGGCCGCCCT TATAAATAAC CGGGCTCAGG AGAAACT

47

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human neurofilament subunit NF-L gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGCGTCAGGA CCTCCCGGCG TATAAATAGG GGTGGCAGAA CGGCGC

46

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human neurokinin-2 receptor (NK-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTCTTCAGC GAAGGGGTTG ATTTATAAGG GTGTTTTCTG CTCTGACA

48

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human n-myc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGGTGTGTCA GATTTTTCAG TTAATAATAT CCCCCGAGCT TCAAAGCGC

49

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase (ODC1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCATGGCGAC CCGCCGGTGC TATAAGTAGG GAGCGGCGTG CCGTGG

46

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ornithine transcarbamylase (OTC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

ATACACAGCG GTGGAGCTTG GCATAAAGTT CAAATGCTCC TACACC

46

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human prepro-oxytocin-neurophysin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC

50

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytochrome P450scc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAG

45

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human p53 gene for transmembrane related p53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CCCCCTCCCAT GTGCTCAAGA CTGGCGCTAA AAGTTTTGAG CTTCTCAAAA

50

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG

47

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT

54

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GCGGGGTGGG CCGGATCAGC TGACTCGCCT GGCTCTGAGC CCCGCCGC

48

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CCGCCGCCGC GCTCGGGCTC CGTCAGTTTC CTCGGCAGCG GTAGGCGAG

49

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for plasminogen activator inhibitor 1 (PAI-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TATTTCTCTGC CCACATCTGG TATAAAAGGA GGCAGTGGCC CACAGAG

47

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human platelet-derived growth factor A-chain (PDGF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

AGGGGCGCGG CGGCGGCGGC TATAACCTC TCCCCGCCGC CGGCC

45

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human PGP9.5 gene for neuron-specific ubiquitin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ACAGTGCCTC TGGCCGGCGC TTTATAGCTG CAGCCTGGCG CTCCGC

46

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human plasminogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC

50

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human phenylethanolamine N-methylase
(PNMT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TCGGGGCGGG GGTGGGGCGG TAGAAAAAAG GGCCGCGAGG CGAGCGGGG

49

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human opiomelanocortin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CTCCCCGTGT GCAGACGGTG ATATTTACCG CCAAATGCGA ACCAGGC

47

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene PRB3L for proline-rich
 protein G1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCCACTGTTC TGCTCCTCTT TATAAAGGGA GCTGCCATGG TTCTCC

46

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human PRB4 gene for proline-rich
 protein Po

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CATTGTTTTG CTCCTCTTTA TAAAGGGAGT TGCCACGTTC CTCC

44

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AGGCTTTGAT ATCAAAGGTT TATAAAGCCA ATATCTGGGA AAGAGA

46

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prothymosin-alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

CCGAGCGCCG CCCACTAATC TATATTAAAG CTTCTGGCGC CGCGTG

46

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human protamine 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TCATAGTGGG CGTCCCCCTT TATATACAAG CTCCCGGGGA GCCTTG

46

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human SPR2-1 gene for small proline
rich protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTGGGTGGGG TAGCAGGCTC TATAAAGAGA TCCTCTGCTG CACGAC

46

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human estrogen-responsive gene pS2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TAAGCAAACA GAGCCTGCCC TATAAAATCC GGGGCTCGGG CGGCCTC

47

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pulmonary surfactant
apoprotein (PSAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AGCCTGGCAG CCCCCACATC TATAAATGCT GCGTCTACCT TACCCT

46

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for prostatic secretory protein PSP-94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGCGTGGTTG CCCTCTCCAG TATAAAAGTT TGATGCAGCT TTTCC

45

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parathyroid hormone-related peptide (PTHrP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAGGTAGACA GACAGCTATG TATATATATG TGGGTTTCGC TACAAGTGG

49

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for purine nucleoside phosphorylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CTGGGGACTC CAGGGCAAGG GATATAAGCC AGAGCCTAGA CCAAGT

46

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human rDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ATTTTGGGCC GCCGGGTTAT

20

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human regenerating protein (reg) gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GTTCTTATCT CAGATCCTGA TATAAAGCTC CTACAGCTAC CTGGCC

46

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human renin gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATCACCCCAT GCATGGAGTG TATAAAAGGG GAAGGGCTAA GGGAGCC

47

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene fragment for retinol binding protein (RBP)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

CGACCCCCTC CCCCCGGCGC TATAAAGCAG CGGGGCGGCC GCGGCG

46

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human serum amyloid A (GSAA1) gene

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:~~

CACCCCGCTA ATTTAAAAA TATATATACA GATATATAGT GGAGATGG

48

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human SAA1 beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

AACCAGCAGG GAAGGCTCAG TATAAATAGC AGCCACCGCT CCCTGGC

47

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene fragment for HLA class II SB 4-beta chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

CTACTTGGGT TCATGGTCTC TAATATTTCA AACAGGAGCT CCCTTTAG

48

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-sis proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TCGCACTCTC CTTTCTCCTT TATAAAGGCC GGAACAGCTG AAAGGG

46

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human SLPI gene for secretory leukocyte protease inhibitor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CACACCCACT GGTGAAAGAA TAAATAGTGA GGTTTGGCAT TGGCCA

46

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human superoxide dismutase (SOD-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

CGAGGCGCGG AGGTCTGGCC TATAAAGTAG TCGCGGAGAC GGGGTG

46

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

TCCATGGCGA CCCGCCGGTG CTATAAGTAG GGAGCGGCGT GCCGT

45

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human steroid 5-alpha-reductase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTGCCCCCGC GCCGCCGCC TATATGTTGC CCGCCGCGGC CTCTG

45

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human substance P receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GTGACGTCTC TGCAGGGGGT TATAAAAGCC TCGTGCGCAG CTAA

44

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human synaptobrevin 1 (SYB1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCGGGAGGCG TGGTCAGCAC TAATAAAGGC GGAGGCCGGC GCGGCA

46

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tyrosine aminotransferase
(TAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

CAACGCCCAT TTGTGGAGAC TATTTAGGA GTTAGGATTT GCATCTG

47

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GACAGATGCA TTCTGTGGGG ATAAATGTC ACAAATTCA TTTCTTT

47

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

TCACAGAGGG CCTGGTCTAG AATATTCCAC ATCTGCTCTC ACTCT

45

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GACAGATGCA TTCTGTGGGG ATAAAATGTC ACAAATTCA TTTCTTT

47

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

TCACAGAGGG CCTGGTCTGG AATATTCCAC ATCTGCTCTC ACTCTG

46

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta chain
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

TGTTACTGTA GGAACACCG TATAAGGACA GGATGTCCCA CCTCC

45

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transferrin (Tf) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

CCGCCCAGGC CGGGAATGGA ATAAAGGGAC GCGGGGCGCC GGAGG

45

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GGGCACCTTG

10

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tissue factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CGGGAGAGCG CGCCGCCGGC CCTTTATAGC GCGCGGGGCA CCGGCTCCCC

50

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transforming growth factor-beta (TGF-beta)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TGCCTTGCCC ATGGGGGCTG TATTTAAGGA CACCGTGCCC CAAGCCC

47

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAGACGTCAT GGGAGGGAGG TATAAAATTT CAGCAGAGAG AAATAGA

47

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CACGTGGTTC AGAGAGAACT TATAAATCTC CCCTCCCCGC GAAGA

45

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase (TH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GGCTTTGACG TCAGCTCAGC TTATAAGAGG CTGCTGGGCC AGGGCT

46

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein gene IIA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TCGTCCCGGC TCTTTCTAGC TATAAACT GCTTGCCGCG CTGCAC

46

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thrombospondin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

CCCAGGAATG CGAGCGCCCC TTATAAAGCG CGCGGCTCCT CCGCCT

46

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human thyroxine-binding globulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ATAATGTTGC TATAACATCT GAATGACAGT CCATGGCATT ATTTC

45

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human thyroglobulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAAAGTGCCA ACGGCAGCTC TATAAAAGCT CCCTGGCCAG GGGACCT

47

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for tumor necrosis factor
(TNF-alpha)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CTCCTCTCGC CCCAGGGACA TATAAAGGCA GTTGTGGCA CACCCA

46

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lymphotoxin (TNF-beta) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCTGCCACTG CCGCTTCCTC TATAAAGGGA CCTGAGCGTC CGGGCC

46

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human type I DNA topoisomerase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

TGACGTCGCC GACGTGTTGT TTAAAAGCGG CCGCGCAGGC GCAGTGAGCC

50

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human triosephosphate isomerase
(TPI) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AGTTCCACTT CGCGGCGCTC TATATAAGTG GGCAGTGGCC GGACTGC

47

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thyroid peroxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATCCAAGCGC AGAGTCAGTT TATAAGGTGG GTAACCAAGT CCCT

44

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GGCCGGGGGC GGGGCCAGGC TATAAACCGC CGGTTAGGGG CCGCCA

46

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human tryptase -I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CGCCCCCTCC TGATCTGGAA GGATAAATGG GGAGGGGAGA GCCACTGGGT

50

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human beta 2 gene for beta-tubulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GCGGAGGCGG GCAGGGAGGG TATATAAGCG TTGGCGGACG GTCGGT

46

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for U 6 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GTATTTTCGAT TTCTTGGCTT TATATATCTT GTGGAAAGGA CGAAAC

46

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human uPA gene for
urokinase-plasminogen activator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GGCGGCGCCG GGGCGGGCCC TGATATAGAG CAGGCGCCGC GGGTCGC

47

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human proto-oncogene vav

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GCAGGCGTGC GGGCGGGTGG GTGGTGGAGG CTGCGA

36

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human vascular cell adhesion
molecule-1 (VCAM1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GCCTCTGCAA CAAGACCCTT TATAAAGCAC AGACTTTCTA TTCA

45

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human vimentin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ACCCTCTTTC CTAACGGGGT TATAAAAACA GCGCCCTCGG CGGGG

45

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human U1 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GTAAAGGGTG AGGTATATGG AGCTGTGACA GGCAGAAGT GTGTGAAGTC

50

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for small nuclear U1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GTAAAGAGTG AGGCGTATGA GGCTGTGTCG GGCAGAGGC CCAAGATCTC

50

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human small nuclear U2 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

TTGAATGTGG ATGAGAGTGG GACGGTGACG GCGGGCGCGA AGGCGAGCGC

50

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human U3 small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

AAAAGTTTGC GGCAGATGTA GACCTAGCAG AGGTGTGCGA GGAGGCCGTT

50

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human U4C small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

AAATGGTAGT CATCATCCGT GGGGGAGCGG GGC GCGAATA AAGCCTTTCC

50

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human histone H3.3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GGGCGGGGCG GCGTGTGTTG GGGGATAGCC TCGGTGTCAG CCATCTTTCA

50

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human histone H4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

AGTTCGGTCC GCCAACTGTC GTATAAAGGC GCTGCCTCAG GTCAGAGGCC

50

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human non-histone chromosomal protein HMG-14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

TGGGGGGCGG CCCGGCCGGC GGGGAGGGGG AGCCGCGGCC GGGACGCGGG

50

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ribosomal protein S14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

AAGTAATAAA CCGTCTTTCC TTATGACGAG TCTTAAACTC TTTGGGAGGA

50

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha tubulin (b
alpha 1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

CGCGACCGAG GGTCTGGGCG TCCCGGCTGG GCCCCGTGTC TGTGCGCACG

50

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human skeletal alpha-actin gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

AGGGAATCGC CCGCGGGCTA TATAAACCT GAGCAGAGGG ACAAGCGGCC 50

- (2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human epidermal 67-kDa Keratin gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GGAAGATCTT GTGTGATAAA ACAATTACCA CATGAACCAA TCTTGCATGC 50

- (2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human 50 KDatype I epidermal keratin gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GACCCGCCCC CTACCCATGA GTATAAAGCA CTCGCATCCC TTTGCAATTT 50

- (2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-1 collagen type I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CTGCTCTCCA TCAGGACAGT ATAAAAGGGG CCCGGGCCAG TCGTCGGAGC 50

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human collagen type-III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GTGAGGGAAG CCAAACTTTT TCCTATTTAA GGCCAAAGCA AAGGAATCTC 50

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pro-alpha-2 (I) mRNA for collagen N-prepropeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

CAGGGAAACT TTTGCCGTAT AAATAGGGCA GATCCGGGAT TTGTTATTTT 50

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibronectin (FN) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

TCCAGAGGGG CGGGAGGGCC GTCCCATATA AGCCCGGCTC CCGCGCTCCG

50

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human von Willebrand factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

TGTTTCCTTT TGGTAATTAA AAGGAGGCCA ATCCCCTGTT GTGGCAGCTC

50

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma
chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA

45

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CAGTCCTGGC TATCCAGGA GCTTACATAA AGGGACAATT GGAGCCTGAG

50

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human involucrin mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

AGGCCAGGCT GCAGAATGAT ATAAAGAGTG CCCTGACTCC TGCTCAGCTC

50

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CCAGACCCTG GCTGCAGACA TAAATAGGCC CTGCAAGAGC TGGCTGCTTA

50

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein B-100 (apoB)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GCTCTTGCAG CCTGGGCTTC CTATAAATGG GGTGCGGGCG CCGGCCGCGC

50

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III
genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TCTAGGGATG AACTGAGCAG

20

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III

genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ACAGGCAGGA GGGTTCTGAC CTGTTTTATA TCATCTCCAG GGCAGCAGGC A

51

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

TACAATTATT GGTAAAGAA GTATATTAGT GCTAATTTC CTCCGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

TACAATTATT GGTAAAGAA GTATATTAGT GCTAATTTC CTCCGTTTGT C

51

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human serum prealbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

CCTAGCTCAG GAGAAGTGAG TATAAAAGCC CCAGGCTGGG AGCAGCCATC

50

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein (AFP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTTTCAGC ATGATTTTCC

50

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human C-reactive protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

AGGCAGGAGG AGGTAGCTCT AAGGCAAGAG ATCTGGGACT T

41

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid
glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC

50

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid
glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC A

51

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

CGGCGCACCA TAAAAGAAGC CGCCCTAGCC ACGTCCCCTC

40

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

CGGCGCACCA TAAAGAAGC CGCCCTAGCC ACGTCCCCTC G

41

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC

50

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC A

51

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-globin germ line gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GTGCCAACAA TGGAGGTGTT TACCTGTCTC AGACCAAGGA CCTCTCTGCA

50

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Chimpanzee gene for alpha-like
zeta-1-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

CCTGGCTGGG CCCAGCTCCC TGTATATAAG GGGACCCTGG GGGCTGAGCA

50

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Chimpanzee gene for alpha-like
zeta-1-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

CCTGGCTGGG CCCAGCTCCC TGTATATAAG GGGACCCTGG GGGCTGAGCA C

51

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha globin gene cluster on chromosome 16: zeta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

CTGGCTGGGC CCAGCTCCCT GTATATAAGG GGACCCTGGG GGCTGAGCAC

50

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human theta 1-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

CCGCGGGACC CCTGGCCGGT CCGCGCAGGC GCAGCGGGGT CGCAGGGCGC

50

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Macaque cynomolgus beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Chimpanzee beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GCAGAAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human germ line gene for beta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Spider monkey (A.geoffroyi)

delta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

CAGGGAGAAC AGGACCAGCA TAAAAGGCAG GGCAGGGCTA ACTGTTGCTT

50

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGGCGGGGCC AGGCTATAAA CCGCCGGTTA GGGGCCGCCA TCCCCTCAGA

50

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-2-adrenergic receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

AGTTCCCCTA AAGTCCTGTG CACATAACGG GCAGAACGCA CTGCGAAGCG

50

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGTGGCAAGC CCATATTTAG GTCTATGAAA ATAGAAGCTG TCAGTGGCTC

50

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human oncogene c-fos

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TTCATAAAAC GCTTGTTATA AAAGCAGTGG CTGCGGCGCC TCGTACTCCA

50

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-myc oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

AATCTCCGCC CACCGGCCCT TTATAATGCG AGGGTCTGGA CGGCTGAGGA

50

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
(bcl-2) proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

CCGCCCCTCC GCGCCGCTG CCCGCCGCC CGCCGCGCTC CCGCCCGCCG 50

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human p53 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ACTCCATTTC CTTTGCTTCC TCCGGCAGGC GGATTACTTG CCCTTACTTG 50

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene homologous to bladder
carcinoma oncogene T24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CGCGGCCCTA CTGGCTCCGC CTCCGCGTT GCTCCCGGAA GCCCGCCCG 50

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-abl gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GGGGCGGGCC TGGCGGGCGC CCTCTCCGGG CCCTTTGTTA ACAGGCGCGT

50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein-i-a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGGCCCTCTT TCCCCTGACC ATAAAAGCAG CCGCTGGCTG CTGGGCCCTA

50

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein I-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ACCCACCCAC CTCCCCGAC TATAAAGGAG CAGCCAGCTC CTGGGCTCCA

50

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human metallothionein-If (MT-IF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

CCCGGCCCCC TCCCTGACT ATCAAAGCAG CGGCCGGCTG TTTGGGTCCA

50

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for 27 Kda heat shock protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

CCCTCAAACG GGTCATTGCC ATTAATAGAG ACCTCAAACA CCGCCTGCTA

50

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human 70 kDa heat shock protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GCGGGTCTCC GTGACGACTT ATAAAACCCC AGGGGCAAGC GGTCCGGATA

50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human macrophage alpha1-antitrypsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

TGCCTCCACC CGAAGTCTAC TTCCTGGGTG GGCAGGAAGT GGGCACTGTG

50

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha1-antitrypsin (S variant) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

CGTTGCCCCT CTGGATCCAC TGCTTAAATA CGGACGAGGA CAGGGCCCTG

50

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human S variable segment 5' of

antithrombin III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

TCTGCCCCAC CCTGTCCTCT GGAACCTCTG CGAGATTTAG AGGAAAGAAC

50

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pulmonary surfactant protein (SP5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CCCCCTCTCCC TACGGACACA TATAAGACCC TGGTCACACC TGGGAGAGGA

50

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Immunoglobulin kappa L-chain V region gene (HK122)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

CCCCCTGCCC TGAAGACTTT TTATAGGCTG GTCACACCCG GAGCAGGAGT

50

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T cell receptor
V-alpha/J-alpha chain (rearranged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TTAAGGTTTG AATCCTCAGT GAACCAGGGC AGAAAAGAAT GATGAAATCC

50

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for HLA-DR alpha heavy
chain (class II antigen)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

TGCATTTTAA TGGTCAGACT CTATTACACC CCACATTCTC TTTTCTTTTA

50

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human MHC class IIHLA-DC-3-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

CTACCACGCA TGGAAACATC CACAGATTTT TATTCTTTCT GCCAGGTACA

50

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor CD3-gamma gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GCCTTCTCTC AAAGGCCCCA GCCCCAACAG TGATGGGTGG AGCCAGTCTA

50

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pregnancy-specific beta-1
glycoprotein mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

CTGCCCTGGG AAGAGGCTCA GCACAGAAAG AGGAAGGACA GCACAGCTGA

50

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pregnancy-specific
beta-1-glycoprotein 5 (PSG5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

AGAGAGGAGG GGACAGAGAG GTGTCCTGGG CCTGACCCCA CCCATGAGCC

50

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human factor VIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

CCTGTGGCTG CTTCCCACTG ATAAAAAGGA AGCAATCCTA TCGGTACTG

50

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ubiquitin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TGACGCAACA CTCGTTGCAT AAATTTGCCT CCGCCAGCCC GGAGCATTTA

50

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human proliferating cell nucleolar protein P120 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ACTATAATAC GCCAAGCGTG CGTTCTGCCG TTCCCTCCGA CACGCGCGAC

50

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for delta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

CAGGGAGGAC AGGACCAGCA TAAAAGGCAG GGCAGAGTCG ACTGTTGCTT

50

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Gorilla fetal A-gamma-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTCCA GCAGTTCCAC

50

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCCAC

50

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Orangutan epsilon-globin gene with flanking Alu repeats

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

CAGAACTTCG GCAGTGAAGA ATAAAAGGCC ACACAGAGAG GCAGCAGCAC

50

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human haptoglobin (Hp1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TAAAAAGACC AGCAGATGCC CCACAGCACT GCTCTTCCAG AGGCAAGACC

50

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human low molecular weight
oligoadenylate synthetase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

AAGACAGCTC CTCCCTTCTG AGGAAACGAA ACCAACAGCA GTCCAAGCTC AGTCAGCAGA 60

AGAGATAAAA G 71

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene fragment for
dihydrofolate reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GGGGGGCGGG GCCTCGCCTG CACAAATAGG GACGAGGGGG CGGGGCGGCC 50

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thymidine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GGCTCGTGAT TGGCCAGCAC GCCGTGGTTT AAAGCGGTCG GCGCGGGACC 50

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human adenosine deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGGGAGGCG GGGCCCGGCC CGTTAAGAAG AGCGTGGCCG GCCGCGGCC

49

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human argininosuccinate synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGCCCCCGGG CCCTGTGCTT ATAACCTGGG ATGGGCACCC CTGCCAGTCC

50

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ornithine aminotransferase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGGGGCGGGG CAGAATCAGC CTTTAAGTTG CAGTGACGCT CCGGCGTCAC

50

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TGACGTCAGC TCAGCTTATA AGAGGCTGCT GGGCCAGGGC TGTGG

45

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human HMG CoA reductase gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

CAGCTCCGAG CGTGCGTAAG GTGAGGGCTC CTTCCGCTCC GCGACTGCGT

50

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human gene for lecithin-cholesterol
 acyltransferase
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CCTAGGGCCC CTCCCACTCC CACACCAGAT AAGGACAGCC CAGTGCCGCT

50

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CGCCCAGAGG GAGGGACCTC CCCTTCGAGG GAGGGCGCCG GAAGTGACGC

50

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GCACAGCACT CCCACTGACA ACTGCCTTGG TCAAGGTGGG CTTTCAGGGCT

50

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human URO-D gene for
uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGGGGGCAGG CTCAGATTCA GGTAAATTG TGGATTGAGC TCGCAGTTAC

50

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human URO-D gene for uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGGGGGCAGG CTCAGATTCA GGTAAATTG TGGATTGAGC TCGCAGTTAC A

51

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human aldolase B (ALDOB) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

AAAAAAAAA CATGATGAGA AGTCTATAAA AATTGTGTGC TACCAAAGAT

50

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG

50

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG A

51

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGTGGGGCGG GCAGGAGCTG CCTTATAACC AGCCCGGGAA CCCCTAGCTC

50

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TGTGGGGCGG GCAGGAGCTG CTTATAACC AGCCCGGGAA CCCCTAGCTC A

51

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC

50

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC G

51

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT

50

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT G

51

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human phosphoglycerate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GAGGCGGGGT GTGGGGCGGT AGTGTGGGCC CTGTTCTCTGC CCGCGCGGTG

50

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for glucose 6-phosphate dehydrogenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

CAGGCGCCCG CCCCCGCCCC CGCCGATTAA ATGGGCCGGC GGGGCTCAGC

50

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human hepatic lipase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT

50

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human hepatic lipase mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT C

51

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human protein C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

AGTGCTGAGG GCCAAGCAAA TATTTGTGGT TATGGATTAA CTCGAACTCC

50

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

CCAGAAGTAA ATACAGCTCA GCTTGACTT TGGTACAAC TATCGACCTT

50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human MHC III HLA factor B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GCAGGTGCCA GAACACAGAT TGTATAAAAG GCTGGGGGCT GGTGGGGAGC

50

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pepsinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

CGATAAGGCG GGACCCAACT TGTATATAAG GGCAGCTCAT GCTGCTGCTC

50

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pepsinogen C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

CGATTAGACT AATCTTGGGC GTATAAAAGA GGAAAGAGTG CCCAGGTCTT

50

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human collagenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

CTGGAAGGGC AAGGACTCTA TATATACAGA GGGAGCTTCC TAGCTGGGAT

50

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human stromelysin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

CCAAACAAAC ACTGTCACTC TTATAAAGCT GCGCTCCCGA GGTGGACCT

50

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

TCTGATCCGT GCAGGGTATT AATGTGTCAG GGCTGAGTGT TCTGAGATT

50

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pancreatic alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

TGTAAAATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT

50

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pancreatic amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

TGTAAAATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT

50

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human cytochrome P450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC

50

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytochrome P-450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC C

51

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for cytochrome P(1)-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

CACGTACAAG CCCGCCTATA AAGGTGGCAG TGCCTTCACC

40

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human steroid 21-hydroxylase [P450
(C21)] B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GGATGGCTGG GGCTCTTGAG CTATAAGTGG CACCTCAGGG CCCTGACGGG

50

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human mitochondrial aldehyde
dehydrogenase 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

TTCCTGACCA TGGTACTTAT AAAAGCAGTG CCGTCTGCCC CATCCATGTC

50

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

AAGGCCATGC AAGTGTGCGG GGGAGCTACA TAAAAGCGCG GGCTCGCGCG

50

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human creatine kinase B isozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

TGGGCGGCCC GCGTTGTGCC CCTTAAGAGC CGCGGGAGCG CGGAGCGGCC

50

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preproenkephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG

50

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preprokephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG G

51

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prepro form of corticotropin releasing factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

TTTTTGAAGA GGGTCGACAC TATAAAATCC CACTCCAGGC TCTGGAGTGG

50

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human preprothyrotropin-releasing hormone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GACCTCACTC GAGCCGCCGC CTGGCGCAGA TATAAGCGGC GGCCCATCTG

50

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCAC-

50

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene coding for ACTH and beta-LPH precursors

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCCACCAGGA GAGCTCGGCA AGTATATAAG GACAGAGGAG CGCGGGACCA

50

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human somatostatin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

TAGCCTGACG TCAGAGAGAG AGTTTAAAAC AGAGGGAGAC GGTGAGAGC

50

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC

50

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC A

51

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

AGGTGGAAAC ACTCTGCTGG TATAAAAGCA GGTGAGGACT TCATTAAGT

50

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TTGAACTGTG GTGCAGGAAA GCCTCAAGTA GAGGAGGGTT GAGGCTTCAA

50

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-LH gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GCCGCCCCCA CAACCCCGAG GTATAAGCC AGATACACGA GGCAGGGGAT

50

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human follicle-stimulating hormone
beta-subunit gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

TAGTTGCACA TGATTTTGTG TAAAAGGTGA ACTGAGATTT CATTGAGTCT

50

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TATTCATGAA GATATCAAAG GTTTATAAAG CCAATATCTG GGAAAGAGAA

50

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parathyroid gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GACATCATCT GTAACAATAA AAGAGCCTCT CTTGGTAAGC AGAAGACCTA

50

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Owl monkey insulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GGGGAGATGG GCTCTGGGCC TATAAGCCA GCAGGGACCC AGCAGCCCTC

50

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human insulin/IGF II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

CCCCGCCTCC AGAGTGGGGG CCAAGGCTGG GCAGGCGGGT GGACGGCCGG

50

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human insulin like growth factor
IGFII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

AAAGAACTCT GCCTTGC GTT CCCCAAATT TGGGCATTGT TCCGGCTCGC 50

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human insulin-like growth factor II
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

CCCTGGGCCG CGGCTGGCGC GACTATAAGA GCCGGGCGTG GGCGCCCGCA 50

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gastrin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

AGTTGGGAGG GACCTTGAGG GCTTTATAAG GCAGGCCTGG AGCATCAAGC 50

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon alpha gene
INF-alpha 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GGAAATCAGT ATGTTCCCTA TTTAAGGCAT CTGCAGGAAG CAAAGCCTTC

50

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for leukocyte interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGAAGCTAGT ATGTTCTTA TTTAAGACCT ATGCACAGAG CAAGGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon alpha gene
INF-alpha 4b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for leukocyte (alpha)
interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GGAAATTAGT ATGTTCACTA TTTAAGGCCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon genes LeIF-L and
LeIF-J

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for fibroblast (beta-1)
interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

ATAGAGAGAG GACCATCTCA TATAAATAGG CCATACCCAC GGAGAAAGGA

50

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-sis gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CTCTCGCACT CTCCCTTCTC CTTTATAAAG GCCGGAACAG CTGAAAGGGT

50

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human migratory inhibitory
factor-related protein 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CAGCTGGCCA AGCCTAACCG CTATAAAAAG GAGCTGCCTC TCAGCCCTGC

50

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human migratory inhibitory
factor-related protein 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTGCCCCAGT CAGGAGCTGC CTATAAATGC CGAGCCTGCA CAGCTCTGGC

50

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human epidermal growth factor related gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GGTCCCTCCT CCTCCCGCCC TGCCTCCCGC GCCTCGGCCC GCGCGAGCTA

50

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human opsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GCTTAGGAGG GGGAGGTCAC TTTATAAGGG TCTGGGGGGG TCAGAACCCA

50

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human blue cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

TTTTGTGGGG TGGGAGGATC ACCTATAAGA GGACTCAGAG GAGGGTGTGG

50

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human red cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

CGGGCTGATC CCACAGGCCA GTATAAAGCG CCGTGACCCT CAGGTGATGC

50

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human green cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

CGGGCTGATC CCACTGGCCG GTATAAAGCG CCGTGACCCT CAGGTGACGC

50

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interferon-inducible gene
IFI-56K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TTGGCTGCTG TTTAGCTCCC TTATATAACA CTGTCTTGGG GTTTAAACGT 50

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interferon-induced 15-Kd
protein (ISG) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GACGTGTGTG CCTCAGGCTT AATAATAGGG CCGGTGCTGC TGCGGAAGCC 50

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ubiquitin-like protein (GdX)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

TCCAGCGCGC GCGCCCGGGG CGGCGGCGCG CGGCGGGGGG TGTTGGGGT 50

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human exogenous retrovirus erv3 5" long terminal repeat

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CCGCCCCCTGT TGGTTGCATG TATAAAAGTC AAGCCCTGTC ATTGTTCAGG

50

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Bovine leukemia virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

ACCTCACCTG CTGATAAATT AATAAAATGC CGGCCCTGTC GAGTTAGCGG

50

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell lymphotropic virus type I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

TCAATAAACT AGCAGGAGTC TATAAAAGCG TGGAGACAGT TCAGGAGGGG

50

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human T-cell leukemia virus II
 proviral LTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TCAAAATAAA AGATGCCGAG TCTATAAAAG CGCAAGGACA GTTCAGGAGG

50

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Human T-cell Lymphotropic virus type
 III (HIV-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCGAGCCCT CAGATCCTGC ATATAAGCAG CTGCTTTTTG CCTGTACTGG

50

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Aids-associated retrovirus
 (arv-2;proviral)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

TGGCGTCCCT CAGATGCTGC ATATAAGCAG CTGCTTTTGG CCTGTACTGG

50

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human immunodeficiency virus type 2 (HIV-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GCCCTCATAT TCTCTGTATA AATATACCCG CTAGCTTGCA TTGTACTTCG

50

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Visna lentivirus, Icelandic strains LV1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CATAACCGCA GATGTAAACA AGTTGCCTAT ATAAGCCGCT TGCTAGCTGG

50

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus strain AD169 gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT

50

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Murine cytomegalovirus
intermediate-early gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GCTGAGCTGC GTTCACGTGG GTATAAGAGG CGCGACCAGC GTCGGTACCG

50

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus
intermediate-early glycoprotein UL37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CGTCATGTCC GGCATCTTCA TGTATATAAG ACGGTGTTTC AAGACGACGT

50

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus I-E
glycoprotein US3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

ACAACGTCAC CAAGAAACGC TATATATTCA AAAACACCGT TCAGTCCACA

50

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TTTGGGGAGG GGAAAGGCGT GGGGTATAAG TTAGCCCTGG CCCGACAGTC

50

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGCCGGCCCC GGCACCACGG GTATAAGGAC ATCCACCACC CGGCCGGTGG

50

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E
gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

AGCCGGCCCC GGTCTGCGG GTATAAGGGC AGCCACGGC CCACTGGGCG

50

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus type I I-E gene
III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

TTCCCGCCGG CCCCTGGGAC TATATGAGCC CGAGGACGCC CCGATCGTCC

50

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E
gene III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CCCCGCGCGC CCCGAGCGAC TATATCAGCC AGGCGACGGG GCGATCGTCC

50

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type 1 I-E
genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GGGGGCGGGT CTCTCCGGCG CACATAAAGG CCCGGCGCGA CCGACGCCCCG

50

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type 2 I-E
genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

ACGGGGGGCG GGCCGTTCTT CGCGCACATA AAGGGCCGGC GTCCCGGTCTG

50

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus DNA
polymerase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG

50

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus b' 2.2 kb transcript (start 160513)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG

50

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus 2.7 kb transcript (start 4578)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GCCCCGCGCTC GGCAGAGCTA CCATATAAAA ACGCAGGGGT TTAGCAGCTT

50

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 82K AlkExo

(start 27048)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CAGCACCAGG AGAGGCTTAA GCTCGGGAGG CAGCGCCACC GACGACAGTA

50

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 42K gene
(start site 106547)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

ATGGGTTGTG GTTATATGCA CTCCTATAA GACTCTCCCC CACGCCCAC

50

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 39k dUTPase
gene (start 106811)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

CGTGTGCGAT AATACACACG CCCATCGAGG CCATGCCTAC ATAAAAGGGC

50

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 33K (start site 145165)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGCCGGGCGA CCCAGATGTT TACTTAAAAG GCGTGCCGTC CGCCGGCATG

50

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 21K (start site 145459)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

CGACGTACGC GATGAGATCA ATAAAAGGGG GCGTGAGGAC CGGGAGGCGG

50

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 5 kb transcript (start 86216)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CCCCACCCCT GCGCGATGTG GATAAAAAGC CAGCGCGGGT GGTTTAGGGT

50

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' RNR2 gene
(start 89774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGTCCGCCTT CTGGTCCACG CATATAAGCG CGGACTAAAA ACAGGGATGT

50

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 RNR2 gene
(start site 247)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

TGGTCCGCCT TCTCGTCCAC GCATATAAGC GCGGCCTGAA GACGGGGATG

50

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tk gene
(start site 47911)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

CGCGGTCCCA GGTCCACTTC GCATATTAAG GTGACGCGTG TGGCCTCGAA

50

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' tk gene
(start site 225)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

CGCGGCCCGA GGTCCACTTC GCATATTAAG GTGACGCGCG TGGCCTCGAA

50

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' dbp gene
(start site 62318)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

CGGCACGCCC CCAGGTAAAG TGTACATATA CCAACCGCAT ACCAGACGCA

50

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gB (3.3
Kb) start 56081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC

50

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gD (start 138337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC

50

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' gD (start 5918)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGAGTATAAT AGAGTCTTTG TGTTTAAAC CCGGGGTCGG TGTGGTGTTC

50

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gE (start site 141171)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GGAGAGGGCC CGCGGCGCAT TTAAGGCGTT GTTGTGTTGA CTTGCCTCT

50

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 ICP gene (start site 58361)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

AATTATTGCT ACGACATCCG TGCTTGTTTG TGTTCCGTGT CTATATCTCT

50

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tr-4 (start site 136729)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GGCGGTGCTG TTTGCGGGTT GGCACAAAAA GACCCCGATC CGCGTCTGTG

50

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 [U-S] b' tr-9
(start 143245)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GTGACGTCAA TTGCCCAGAGG CGCATAAAGG GCCGGTGGTC CGCCTAGCCG

50

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' VP5
(start 40768)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGGGTGGGGC GGGGGGGGGG GTATATAAGG CCTGGGATCC CACGTCCCCG

50

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.1kb
transcript (start 26639)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

CCCGTTAACC CCCCACGTGA TCAGCACGCC ACCGACACCG CAGACGAAAA

50

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g'
a'TIF/VSP (start 105259)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GGGGCGGCCC GTGCGGGTTG CTAAATGCG TGGTGGCGAC CACGGGCTGT

50

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.7 kb
transcript (start 100998)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GCCACGCCCA TAAGCTCCTC CCGATAAAAA GCGCCCCGAT GGCCCTGGAC

50

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus UL36 gene
(start 49862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GACGTCAACG CTGATAGTGT CTATAAAGGC CGTGCCGCCG CGCCGTAGTT

50

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp65 gene
(start 121072)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TCCGCGTTTG GTCGCCTGCC TATGTAAGGC GGCGGCCGCA GAGGGCGCGC

50

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp71 gene
(start 119223)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTCACCGCTG CTATATTTGC GACAGTTGCC GGAACCC TTC CCGACCTCCC

50

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp150 gene
(start 43092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

CGTATCCGCC TCCGCTATTA AACTACCCCC CCTCCCTCTA GGTGGGGCGC

50

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 5 Kb
transcript (start 103313)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

TTGTGTCGCA GGGCGGCCCCG CGTATAAAGG CGAGAGCGCG GGACCGTTTC

50

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gC (start
96170)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

AACCCCGGAT GGGGCCCCGGG TATAAATTCC GGAAGGGGAC ACGGGCTACC

50

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 g' gC (start 670)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

CGGGGGGTGC CGTGGACGGG TATAAAGGCC AGGGGGGCAC GCGGGCCCAT

50

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gH gene (start 46581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

CGGCAATAAA AAGACAGAAT AAAACGCACG GGTGTTGGGT CGTTTGTTC

50

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 42 K (start site 107130)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

CCGGAGTCCC CGCTAACCTT CGGCATAAAA GCCACCGCGC GCCTGTTGAC

50

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 Ori_s ORF
(start site 132287)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CGGAGGCCCC CGGGGTGCGT CCCCTGTGTT TCGTGGGTGG GGTGGGCGGG

50

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 18 K (start site 97951)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

CCCGCCACC GCTGGGCGCT ATAAAGCCGC CACCCTCTCT TCCCTCAGGT

50

(2) INFORMATION FOR SEQ ID NO:537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 18K (start site 2391)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CCCCGCCGTC CCCCAGGCGT TATAAGCCGC CGCACTCGCT TTTCCCACCG

50

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus L1 1Kb gene
(start site 103194)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TGGTGCCTTG GCTTTAAAGG GGAGATGTTA GACAGGTAAC TCACTAAACA

50

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 145K gene
(start site 1721)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

ACTGTATAAA GGTAAGTATT ATTAAATTTT AGAGACACTA TCACGTGTAA

50

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 20K (start site 9660)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

CTTTTAGCCA TGCCATGCTC TATAAATCAC TTCCCTATCT CAGGTAGGCC 50

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [DL/R] (start site 52787)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

ACAGAGACCC CAAAAGAGG ATAAAGAAG GCGAGCCGGC CCGGCTCGCC 50

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 61372)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GTGACGGTCA GGCAGCTCCT GTATTAACT TTGCGGACAG AGGCCAGAGC 50

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 57050)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

TAATTACGCT TGTGTACATA TTAAATCCA CACAAGTGGC CAGAGTGGGC

50

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 (start site 88539)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GACAGGGACG GCGGCGCTAT ATATAAGAGC CCAAGACCCG GCTCTCTTTA

50

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 88897)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

CGGATTAGAT GGGGATATTT AAAAGGGGCA GCAATCTCGG CTGTTTGTAC

50

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 90021)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

ACCCAACAGG TGGTGAAAAT ATAACACAGG TGACACCAGC CTCTATCAGC

50

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-L] L1 (start site 92157)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

ACCCCCCTTG TACCTATTAA AGAGGATGCT GCCTAGAAAT CGGTGCCGAG

50

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-L] L3 (start site 88480)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

CGGGTCTTGG GCTCTTATAT ATAGCGCCGC CGTCCCTGTC TGTTAGATCA

50

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-K] 2.1 Kb
(start site 109939)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

AGACGCCCTC AATCGTATTA AAAGCCGTGT ATTCCCCCGC ACTAAAGAAT

50

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-K] 1.3kb
transcript (start 110632)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TTGCGACCCC TCTGATATTA AGGTGGTTAT TTTGGGCCAG GACCCCTATC

50

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-H] L1
(start site 137680)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGTGCCCCG ACTCAGAATT ATTAAACCGG GTGGCAGCTC CTGGCAGTCA

50

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1
(start site 159337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

AAGGGCAGGG GGTGGGTATT TAAGGATCTA TATGCCCTTC TCTACCTGCA

50

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] R1
(start 165496)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

AATGGGCGTG GCAGAATAGT ATAAGACGCG AGGCCTGGGT GAGGAGAGTC

50

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L2
(start 167495)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TCTTTCCTTG TCCTTACTGT ATAAAAGTCC ACGAAAACAG CTGTGCCTCA 50

(2) INFORMATION FOR SEQ ID NO:555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EcoR1-D] L1A
start 169165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ACTGATGAGT AAGTATTACA CCCTTTGCCC CACACCCCCT TTCCCTTACT 50

(2) INFORMATION FOR SEQ ID NO:556:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EBNA] E1 (start
site 11333)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

AGGGGGGGAC TAAGGTCCCA CTACAAAAAC TCTGTGTTCT GCTGCAAATT 50

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EBNA] E2 (start site 14399)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GGTATAAAGT GGTCTGCAG CTATTTCTGG TCGCATCAGA GCGCCAGGAG

50

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1 (start site 169514)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

CTCTGACGTA GCCGCCCTAC ATAAGCCTCT CACACTGCTC TGCCCCCTTC

50

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type 2 E1a (start 498)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GTCAGCTGAC GCGCAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 E1a (start 499)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GTCAGCTGAC GTGTAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-7 E1a (start site 512)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TCAGCTGATC GCTAGGGTAT TTAAACCTGA CGAGTTCCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-12 E1a (start site 306)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAATTGATGA CGGCAATTTT ATTATAGGCG CGGAATATTT ACCGAGGGCA

50

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-12 E1a (start site 445)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GTCAGCTGAT CGTTTGGGTA TTTAATGCCG CCGTGTCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Simian Adenovirus SA7 E1a (start site 440)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

TTATTGTCTA GGTGAGGGTA TTAAACCGG CTCAGACCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 E1b (start 1700)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC 50

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 E1b (start site 1703)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC 50

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 E1b (start site 1577)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TTCTTGGGTG GGGTCTTGGA TATATAAGTA GGAGCAGATC TGTGTGGTTA 50

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-12 E1b (start site 1527)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TGGGCGTGGT TAAACAGGGA TATAAAGCTG GGTGTTGTT GCTTTGAATA 50

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 EII (start site 27092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAAAGGGCGC GAAACTAGTC CTTAAGAGTC AGCGCGCAGT ATTTGCTGAA - 50

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIII (start site 27610)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TGCGGTGCGC CGGGCAGGGT ATAACCTACC TGAAAATCAG AGGGCGAGGT 50

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-5 EIII (start site 239)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

TGCGGTCGCC CGGGCAGGGT ATAAC TACC TGACTCTTGG AGGGCGAGGT 50

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIV (start site 35611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

TTACGTCATT TTTTAGTCCT ATATATACTC GCTCTGTACT TGGCCCTTTT 50

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 IVa2 (start site 5827)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTCGTCTC

50

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-5 IVa2 (start site 5837)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTTGTCTC

50

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-7 IVa2 (start site 5692)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CCCTCCCACG TGGCCTCCTT TGTGCTGGCC TGGACACGCG CTTTTGTATC

50

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-2 IX (start site 3575)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTCAT GTAGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 IX (start site 3581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTTAT GTAGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-7 IX (start site 3460)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ATGGGGACTT TCAGGTTGGT AAGGTGGACA AATTGGGTAA ATTTTGTTAA

50

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 major late (start site 6039)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GTGTTCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-5 major late (start site 6049)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GTGTTCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-7 major late (start site 5904)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GGGTCCCCGC CGGGGGGGTA TAAAAGGGGG CGGACCTCTG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-12 major late
(start site 972)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

AATTTTCTGG TGGTGGGCTA TAAAAGGGG CGGGTCCTTG GTCTTCATCG

50

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-2 LIIa (start site
25954)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCGTGGTAG TCCTCAGGTA CAAATTGCG AAGGTAAGCC GACGTCCACA

50

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type 18 E6
gene (start site 30)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CAGCACATAC TATACTTTTC ATTAATACTT TTAACAATTG TAGTATATAA

50

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type-16 E6/E7
(start site 97)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAACCGAAAC CGGTTAGTAT AAAAGCAGAC ATTTTATGCA CCAAAGAGA

50

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type-18 E6
(start site 105)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GGACCGAAAA CGGTGTATAT AAAAGATGTG AGAAACACAC CACAATACTA

50

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1[+.04] (start

site 209)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

AGTGGGCGTG GCTAACTGTA TATAAGCAGT CACTCTGGTC GGTTACTCAC

50

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1 [+40] (start
site 2010)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GCCGAAGCTA GACACTCCTA TAAATTCGCT AGGTTCAATG CGCTCACCAT

50

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parvovirus B19-Au B19 [0.06]
(start site 347)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAGCGTAGGC GGGGACTACA GTATATATAG CACGGTACTG CCGCAGCTCT

50

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CCGCCCCCTAA CTCCGCCAG TTCCGCCAT TCTCCGCCCC ATGGCTGACT

50

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t early P2 (start site 5233)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT

50

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BK virus T/t early (start site 99)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CCTGTGGCCT TTTTTTTTAT AATATATAAG AGGCCGAGGC CGCCTCTGCC

50

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Polyoma virus T/t E (start site 156)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GGCCACCCAA ATTGATATAA TTAAGCCCCA ACCGCCTCTT CCCGCCTCAT 50

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Simian virus 40 late (start site 325)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GTTCTTTCCG CCTCAGAAGG TACCTAACCA AGTTCCTCTT TCAGAGGTTA 50

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 3.6kb P1 (start 1659)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AGTTGGGGGA GGAGATTAGG TTAAAGGTCT TTGTACTAGG AGGCTGTAGG 50

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 3.6 kb
P2 (start 1690)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

TGTACTAGGA GGCTGTAGGC ATAAATTGGT CTGTTACCA GCACCATGCA

50

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2
kb-P1 (start 3061)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

ATCGGCAGTC AGGAAGACAG CCTACTCCCA TCTCTCCACC TCTAAGAGAC

50

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2
kb P2 (start 3092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

CTCTCCACCT CTAAGAGACA GTCATCCTCA GGCCATGCAG TGGAACTCCA

50

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-F] R1
(start 58862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TATTTTGTGAA AAGGGATATT ATAAAACAGG TCATTGCTCG GATTGTGGCA

50

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Promoter Sequence of IL-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GGTGTGAGGC GTCACCACTT GGGCCTATAA AAGCTGCCAC AAGACGCCAA GGCCAC

56

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, higher
affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

CGTTCGCACT T

11

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, lower
affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

TGCTCGCACT T

11

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9Z1 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GCGCGCGCGC GTTCGCACTT CCGCCGCCCG

30

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9Z2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GGCGCCGGCC GTTCGCACTT CGCGCGCGCG

30

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 CCCG TEST SEQ. / UL9 ASSAY
SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGCCCGCCCC GTTCGCACTT CCCGCCCCGG

30

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 GGC TEST SEQ. / UL9 ASSAY

SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGCGGGCGCC GTTCGCACTT GGGCGGGCGG

30

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 ATAT TEST SEQ. / UL9 ASSAY
SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GGATATATAC GTTCGCACTT TAATTATTGG

30

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 polyA TEST SEQ. / UL9 ASSAY
SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GGAAAAAAAC GTTCGCACTT AAAAAAAGG

30

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: UL9 polyT TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GGTTTTTTTTC GTTCGCACTT TTTTTTTTGG

30

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: UL9 GCAC TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGACGCACGC GTTCGCACTT GCAGCAGCGG

30

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: UL9 ATori-1 Test sequence / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GCGTATATAT CGTTCGCACT TCGTCCCAAT

30

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: oriECO2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GGCGAATTCG ACGTTCGCAC TTCGTCCCAA T

31

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: oriECO3 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GGCGAATTCG ATCGTTCGCA CTTCGTCCCA AT

32

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: WILD TYPE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

AAGTGAGAAT TCGAAGCGTT CGCACTTCGT CCCAAT

36

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: TRUNCATED UL9 BINDING SITE, COMPARE
SEQ ID NO:601

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TTCGCACTT

9

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HSVB1/4, SEQUENCE OF COMPETITOR DNA
MOLECULE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGTCGTTTCGC ACTTCGC

17

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 14B, top strand of an exemplary target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HSV primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

ATTGGGACGA AG

12

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: a sample distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

TTCCTCCTTT C

11

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: a distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TTCCNNNTTT C

11

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27A, test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27B, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GCGTANNNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27C, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GCGTANNNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27D, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GCGTANNNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: -35 region consensus sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TTGACA

6

- (2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: -10 region consensus sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

TATAAT

6

- (2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HIV-1, LTR sequence, Figure 28

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GTTAGAGTGG AGGTTTGACA GCCGCCTAGC ATTTTCATCAC ATGGCCCGAG AGCTGCATCC	60
GGAGTACTTC AAGAACTGCT GACATCGAGC TTGCTACAAG GGACTTTCCG CTGGGGACTT	120
TCCAGGGAGG CGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT CCTGCATATA	180
AGCAGCTGCT TTTTGCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC	240
TC	242

- (2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: a TFIID binding site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

CCTGCATA

8

(2) INFORMATION FOR SEQ ID NO:629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: a TFIID binding site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AAGCAGCT

8

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCAGAATTCT GCAG

14

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GCAGAATTCT GCAGCGTTCTG CACTTTCTAG AGCTCAGG

38

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AGATCTCGAG TCC

13

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GCAGAATTCT GCAGNNNNCG TTCGCACTTT CTAGAGCTCA GG

42

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCAGAATTCT GCAGNNNNNN NNCGTTGCA CTTTCTAGAG CTCAGG

46

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GCAGAATTCT GCAGCGTTTCG CACTTNNNNN NNNTCTAGAG CTCAGG

46

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

CGTGAATTCT GCAG

14

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

CGTGAATTCT GCAGATG

17

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CGTGAATTCT GCAGATGAGG TACCNMNMNN CGTTCGCACT TTCTAGAGCT CTCC

54

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GTGAAAGATC TCGAGAGG

18

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AAGATCTCGA GAGG

14

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oris

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

CGTTTCTCACT T

11

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Trimeric test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ACGTACGTAC GT

12

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

ACGTTTCGCA CTTAGCT

17

(2) INFORMATION FOR-SEQ ID NO:644: -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

ACGATTCGCA CTTAGCA

17

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

AGCCTTCGCA CTTAGCC

17

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

AGCGTTCGCA CTTAGCG

17

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

TGCTTTTCGCA CTTTGCT

17

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

TGCATTCGCA CTTTGCA

17

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

TGCCTTCGCA CTTTGCC

17

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

TGCGTTCGCA CTTTGCG

17

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CCATTTCGCA CTTCCAT

17

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CCCTTTCGCA CTTCCCT

17

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

CCGTTTCGCA CTTCCGT

17

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCTTTTCGCA CTTCCCTT

17

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

TTCCNTTCC

9

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTCCNNTTCC

10

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

TTCCNNNTTC C

11

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

TTCCNNNNTT CC

12

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

CGTTCGCACT TTTAC

15

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CGTTCGCACT TTACN

15.

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

CGTTCGCACT TACNN

15

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

CCCGGGTTAC

10

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

CCCGGGTACN

10

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

CCCGGGACNN

10

452

435